```
                                                M   S   P   S   P   T   A   L   F   C   L      11
GGAGTCGACCCACGCGTCCGCAGGGCTGAGGAACC ATG TCT CCA TCC CCG ACC GCC CTC TTC TGT CTT      68

 G   L   C   L   G   R   V   P   A   Q   S   G   P   L   P   K   P   S   L   Q      31
GGG CTG TGT CTG GGG CGT GTG CCA GCG CAG AGT GGA CCG CTC CCC AAG CCC TCC CTC CAG     128

 A   L   P   S   S   L   V   P   L   E   K   P   V   T   L   R   C   Q   G   P      51
GCT CTG CCC AGC TCC CTG GTG CCC CTG GAG AAG CCA GTG ACC CTC CGG TGC CAG GGA CCT     188

 P   G   V   D   L   Y   R   L   E   K   L   S   S   S   R   Y   Q   D   Q   A      71
CCG GGC GTG GAC CTG TAC CGC CTG GAG AAG CTG AGT TCC AGC AGG TAC CAG GAT CAG GCA     248

 V   L   F   I   P   A   M   K   R   S   L   A   G   R   Y   R   C   S   Y   Q      91
GTC CTC TTC ATC CCG GCC ATG AAG AGA AGT CTG GCT GGA CGC TAC CGG TGC TCC TAC CAG     308

 N   G   S   L   W   S   L   P   S   D   Q   L   E   L   V   A   T   G   V   F     111
AAC GGA AGC CTC TGG TCC CTG CCC AGC GAC CAG CTG GAG CTC GTT GCC ACG GGA GTT TTT     368

 A   K   P   S   L   S   A   Q   P   G   P   A   V   S   S   G   G   D   V   T     131
GCC AAA CCC TCG CTC TCA GCC CAG CCC GGC CCG GCG GTG TCG TCA GGA GGG GAC GTA ACC     428

 L   Q   C   Q   T   R   Y   G   F   D   Q   F   A   L   Y   K   E   G   D   P     151
CTA CAG TGT CAG ACT CGG TAT GGC TTT GAC CAA TTT GCT CTG TAC AAG GAA GGG GAC CCT     488

 A   P   Y   K   N   P   E   R   W   Y   R   A   S   F   P   I   I   T   V   T     171
GCG CCC TAC AAG AAT CCC GAG AGA TGG TAC CGG GCT AGT TTC CCC ATC ATC ACG GTG ACC     548

 A   A   H   S   G   T   Y   R   C   Y   S   F   S   S   R   D   P   Y   L   W     191
GCC GCC CAC AGC GGA ACC TAC CGA TGC TAC AGC TTC TCC AGC AGG GAC CCA TAC CTG TGG     608

 S   A   P   S   D   P   L   E   L   V   V   T   G   T   S   V   T   P   S   R     211
TCG GCC CCC AGC GAC CCC CTG GAG CTT GTG GTC ACA GGA ACC TCT GTG ACC CCC AGC CGG     668

 L   P   T   E   P   P   S   S   V   A   E   F   S   E   A   T   A   E   L   T     231
TTA CCA ACA GAA CCA CCT TCC TCG GTA GCA GAA TTC TCA GAA GCC ACC GCT GAA CTG ACC     728

 V   S   F   T   N   K   V   F   T   T   E   T   S   R   S   I   T   T   S   P     251
GTC TCA TTC ACA AAC AAA GTC TTC ACA ACT GAG ACT TCT AGG AGT ATC ACC ACC AGT CCA     788

 K   E   S   D   S   P   A   G   P   A   R   Q   Y   Y   T   K   G   N   L   V     271
AAG GAG TCA GAC TCT CCA GCT GGT CCT GCC CGC CAG TAC TAC ACC AAG GGC AAC CTG GTC     848

 R   I   C   L   G   A   V   I   L   I   I   L   A   G   F   L   A   E   D   W     291
CGG ATA TGC CTC GGG GCT GTG ATC CTA ATA ATC CTG GCG GGG TTT CTG GCA GAG GAC TGG     908

 H   S   R   R   K   R   L   R   H   R   G   R   A   V   Q   R   P   L   P   P     311
CAC AGC CGG AGG AAG CGC CTG CGG CAC AGG GGC AGG GCT GTG CAG AGG CCG CTT CCG CCC     968

 L   P   P   L   P   Q   T   R   K   S   H   G   G   Q   D   G   G   R   Q   D     331
CTG CCG CCC CTC CCG CAG ACC CGG AAA TCA CAC GGG GGT CAG GAT GGA GGC CGA CAG GAT    1028

 V   H   S   R   G   L   C   S   •                                                 340
GTT CAC AGC CGC GGG TTA TGT TCA TGA                                             1055
```

FIGURE 1

CCGCTGAACCCCAGGCACGGTCGTATCCAAGGGAGGGATCATGGCATGGGAGGCGACTCAAAGACTGGCGTGTGTGGAG 1134

CGTGGAAGCAGGAGGGCAGAGGCTACAGCTGTGGAAACGAGGCCATGCTGCCTCCTCCTGGTGTTCCATCAGGGAGCCG 1213

TTCGGCCAGTGTCTGTCTGTCTGTCTGCCTCTCTGTCTGAGGGCACCCTCCATTTGGGATGGAAGGAATCTGTGGAGAC 1292

CCCATCCTCCTCCCTGCACACTGTGGATGACATGGTACCCTGGCTGGACCACATACTGGCCTCTTTCTTCAACCTCTCT 1371

AATATGGGCTCCAGACGGATCTCTAAGGTTCCCAGCTCTCAGGGTTGACTCTGTTCCATCCTCTGTGCAAAATCCTCCT 1450

GTGCTTCCCTTTGGCCCTCTGTGCTCTTGTCTGGTTTTCCCCAGAAACTCTCACCCTCACTCCATCTCCCACTGCGGTC 1529

TAACAAATCTCCTTTCGTCTCTCAGAACGGGTCTTGCAGGCAGTTTGGGTATGTCATTCATTTTCCTTAGTGTAAAACT 1608

AGCACGTTGCCCGCTTCCCTTCACATTAGAAAACAAGATCAGCCTGTGCAACATGGTGAAACCTCATCTCTACCAACAA 1687

AACAAAAAAAACACAAAAATTAGCCAGGTGTGGTGGTGCATCCCTATACTCCCAGCAACTCGGGGGGCTGAGGTGGGAGA 1766

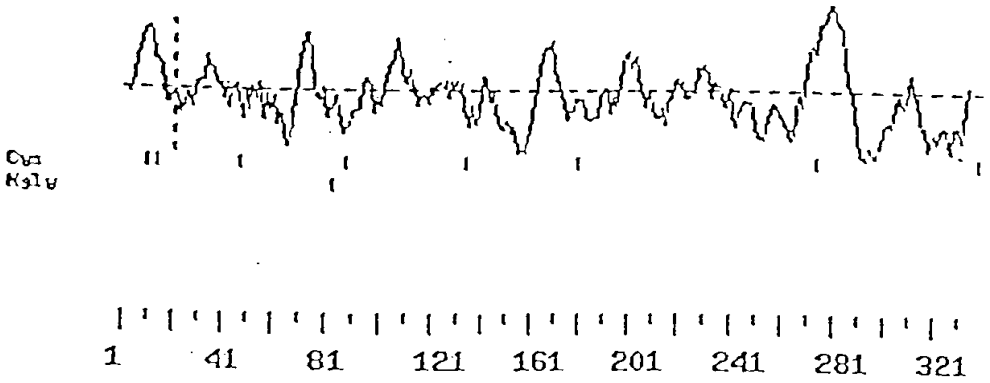
ATGGCTTGAGCCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATCACACCACTGCACTCTAGCTCGGGTGACGAAGCCTGA 1845

CCTTGTCTCAAAAAATACAGGGATGAATATGTCAATTACCCTGATTTGATCATAGCACGTTGTATACATGTACTGCAAT 1924

ATTGCTGTCCACCCCATAAATATGTACAATTATGTATACATTTTTAAAATCATAAAAATAAGATAATGAAAAAAAAAAA 2003

AAAAAAAAAAAAAAAGGGCGGGCCGCTAGACTAGTCTAGAGAACA 2047

FIGURE 1 cont.



MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLE
KLSSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP
GPAVSSGGDVTLQCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPIITVTAAHSGTYRC
YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT
TETSRSITTSPKESDSPAGPARQYYTKGNLVRICLGAVILIILAGFLAEDWHSRRKRLRH
RGRAVQRPLPPLPPLPQTRKSHGGQDGGRQDVHSRGLCS

FIGURE 2

```
ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> U91928 ORF                                              1893 aa vs.
> hT268 ORF                                               1017 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
37.7% identity;          Global alignment score: -8

                10        20        30        40        50        60        70
inputs ATGACGCCCGCCCTCACAGCCCTGCTCTGCCTTGGGCTGAGTCTGGGCCCCAGGACCCGCGTGCAGGCAG
       :::.: ::  :::  :: :::::  :::: :::::::::.:::::::: :  .: .:: ::  :::::. .:
       ATGTCTCCATCCCCGACCGCCCTCTTCTGTCTTGGGCTGTGTCTGGGGCG-TGTGCCAGC--GCAGAGTG
                10        20        30        40        50          60

                80        90       100       110       120         130
inputs GGCCCTTCCCCAAACCCACCCTCTGGGCTGAGCCAGGCTCTGTGAT-CAGCTGGGGGAGCCCCGTGACCA
       :.::  :::::::.:::.:::::  .:::: .::: .::::  ::.: :  :::::.:.::::  ::::::
       GACCGCTCCCCAAGCCCTCCCTCCAGGCTCTGCCCAGCTCCCTGGTGCCCCTGGAGAAGCCA-GTGACCC
        70        80        90       100       110       120         130

     140       150       160       170       180       190       200
inputs TCTGGTGTCAGGGGAGCCTGGAGGCCCAGGAGTACCGACTGGATAAAGAGGGAAGCCCAGAGCCCTTGGA
       :: :::: :::::  .:::      ::.:: ::.  :::  :..          ::: .:::     ...
       TCCGGTGCCAGGG--ACCT------CCGGGCGTG--GACCTGTA--------CCGCCTGGAG-----AAG
        140         150         160         170               180

    210       220       230       240       250       260       270
inputs CAGAAATAACCCACTGGAACCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCG
       :.::..:  :: .:.:::.::: :.:::.:: ::: .   ::: :::::::. :::::: .... . :. ::
       CTGAGTT--CCAGCAGGTACC-AGGATCA-GGCAGTCCTCTTCATCCCGGCCATGAAGAGAAGTCTGGCT
           190         200         210       220       230       240

    280       290       300       310       320       330       340
inputs GGGAGATACCGCTGCCACTATTACAGCTCTGCAG--GCTGGTCAGAGCCCAGCGACCCCCTGGAGCTGGT
       ::. : :::::::::  :::   ::: .: : ::   ::::::  .:::::::::::  :::::::: ::
       GGACGCTACCGCTGCTCCTAC--CAGAACGGAAGCCTCTGGTCCCTGCCCAGCGACCAGCTGGAGCTCGT
    250       260       270       280       290       300       310

       350       360       370       380       390       400       410
inputs GATGACAGGATTCTACAACAAACCCACCCTCTCAGCCCTGCCCAGCCCTGTGGTGGCCTCAGGGGGGAAT
        .  ::.::: : :. . ::::::::.: ::::::::::.::::.:::: : :::: : :::::.:::.:
       TGCCACGGGAGTTTTTGCCAAACCCTCGCTCTCAGCCCAGCCCGGCCCGGCGGTGTCGTCAGGAGGGGAC
       320       330       340       350       360       370       380

       420       430       440       450       460       470       480
inputs ATGACCCTCCGATGTGGCTCACAGAAGGGATATCACCATTTTGTTCTGATGAAGGAAGGAGAACACCAGC
       .:.::::: :..::: . .:.:.:.: :: :.: ::::.:::: :::::.. ::::::::
       GTAACCCTACAGTGTCAGACTCGGTATGGCTTTGACCAATTTGCTCTGTACAAGGAAGG-----------
       390       400       410       420       430       440

       490     , 500       510       520       530       540       550
inputs TCCCCCGGACCCTGGACTCACAGCAGCTCCACAGTGGGGGGTTCCAGGCCCTGTTCCCTGTGGGCCCCGT
       ::::::::                                :   ::::::.                :..
```

FIGURE 3

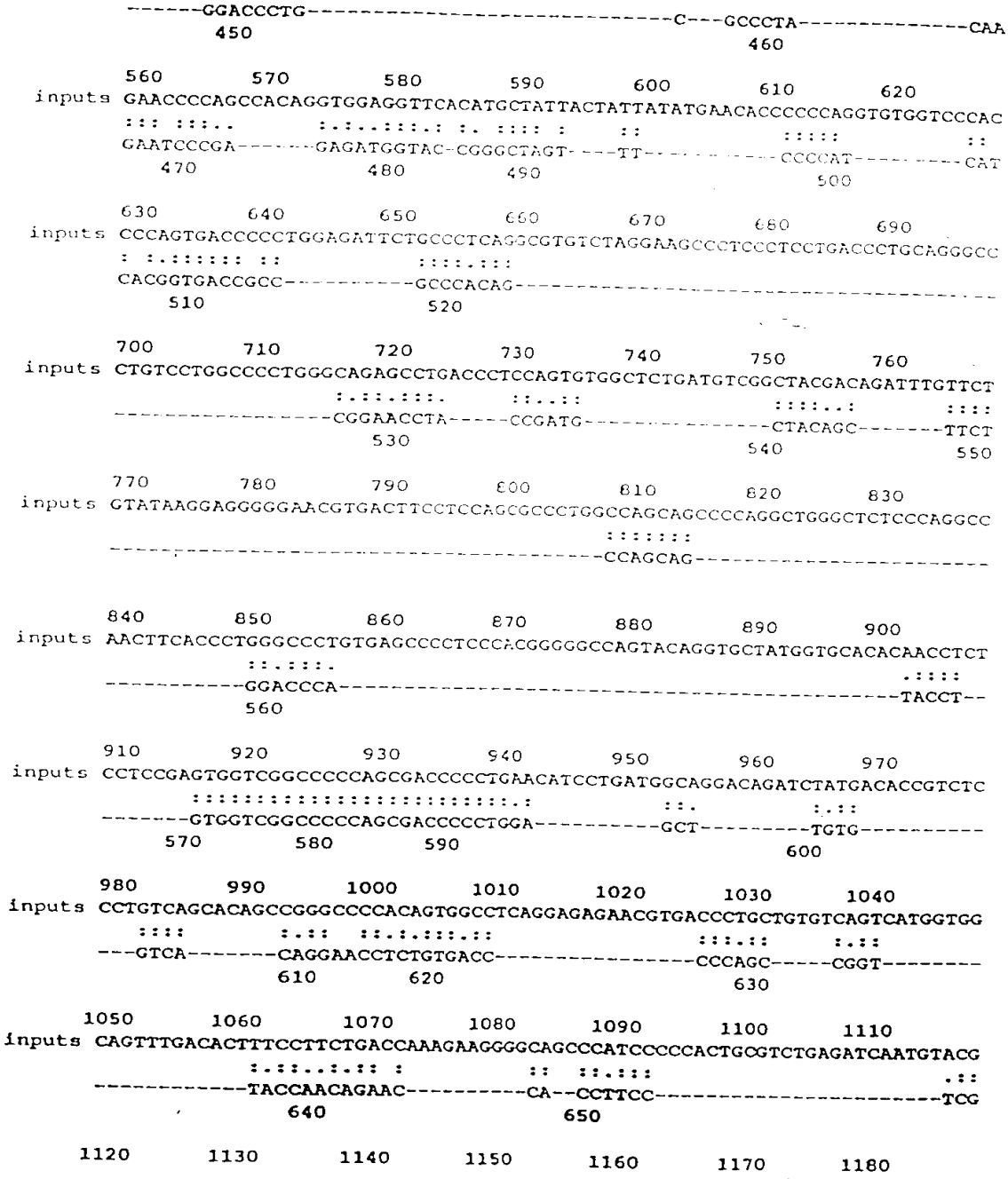


FIGURE 3 cont.

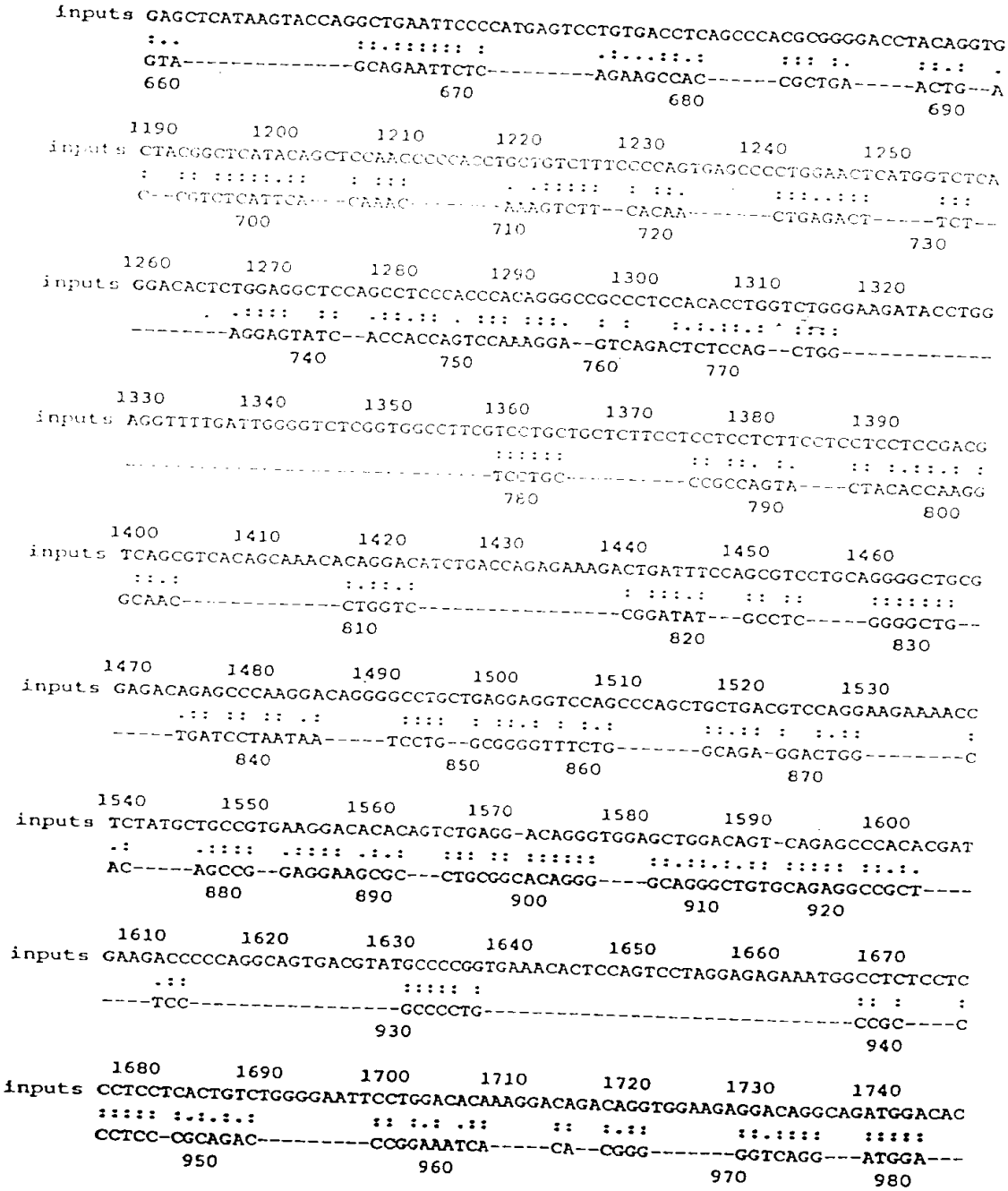


FIGURE 3 cont.

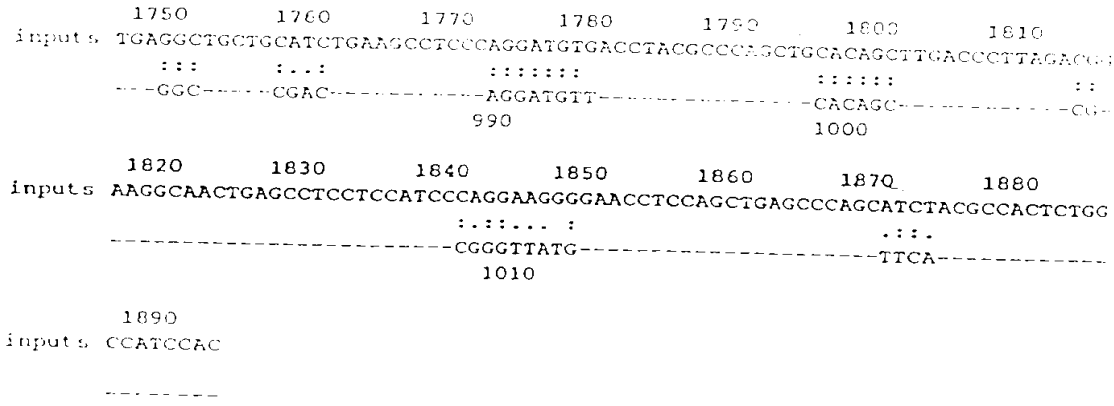


FIGURE 3 cont.

```
ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> hT268 a.a.                                        339 aa vs.
> GenPept U91928 - Human clone HL9 monocyte inhib   631 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
23.0% identity;          Global alignment score: -642

                10        20        30        40        50        60
inputs MSPSFTALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLEKLSSS----
       :.:. :::.:::: :: :. .:.::.:::.: : :.:...   :::..::::.  .. :::.: .:.
       MTPALTALLCLGLSLGPRTRVQAGPFPKPTLWAEPGSVISWGSPVTIWCQGSLEAQEYRLDKEGSPEPLD
                10        20        30        40        50        60        70

                70        80        90       100       110       120       130
inputs RYQ-----DQAVLFIPARKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDV
       : .     ..: . ::.:    :::::: : ... :: :::.:::: :: ..::.::: :.:.:.:::..
       RNNPLEPKNFARFSIPSMTEHHAGRYRCHYYSSAGWSEPSDPLELVMTGFYNKPTLSALPSPVVASGGNM
                80        90       100       110       120       130       140

inputs TLQCQT-------------------- ------------------------------EY----------
       ::.: .                                                    :.
       TLRCGSQKGYHNFVLMKEGEHQLPRTLDSQQLHSGGFQALFPVGPVNPSHRWEFTCYYYYMNTPQVWSHP
              150       160       170       180       190       200       210

                                                 140       150
inputs ------------------------------------------GFDQFALYKEGDP--------------------
                                                 :.:.:.:::::.
       SDPLEILPSGVSRKPSLLTLQGPVLAPGQSLTLQCGSDVGYDRFVLYKEGERDFLQRPGQQPQAGLSQAN
              220       230       240       250       260       270       280

                                                                          160
inputs -----------APYK----------------NP-----------------------------------ERW--
                 ..:.                .:                                    . :
       FTLGPVSPSHGGQYRCYGAHNLSSEWSAPSDPLNILMAGQIYDTVSLSAQPGPTVASGENVTLLCQSWWQ
              290       300       310       320       330       340       350

                                        170       180       190       200
inputs --------------------------YRASFPIITVTAAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTG
                                  :.: ::.  ::.::.::::::.  : .: : : ::.::::.:.:
       FDTFLLTKEGAAHPPLRLRSMYGAHKYQAEFPMSPVTSAHAGTYRCYGSYSSNPHLLSFPSEPLELMVSG
              360       370       380       390       400       410       420

     210       220       230                 240       250       260
inputs TSVTPSRLPTEPPSS--VAEFSEATAELTVSFTNKVF---------TTETSRSITTSPKESD--SPAGPA-
       :  .:  :: :::.  .. . :.  ..:.:.  .:           :.  :.... .:   :::.:
       HSGGSSLPPTGPPSTPGLGRYLEVLIGVSVAFVLLLFLLLFLLLRRQRHSKHRTSDQRKTDFQRPAGAAE
              430       440       450       460       470       480       490

              270       280       290
inputs RQYYTKGNLVRICLGAVIL-----IILAGFLAEDW----------------------HSRRKR--------
       .   .: : :   .: .        . .  .::.                      ::  .:
```

FIGURE 4

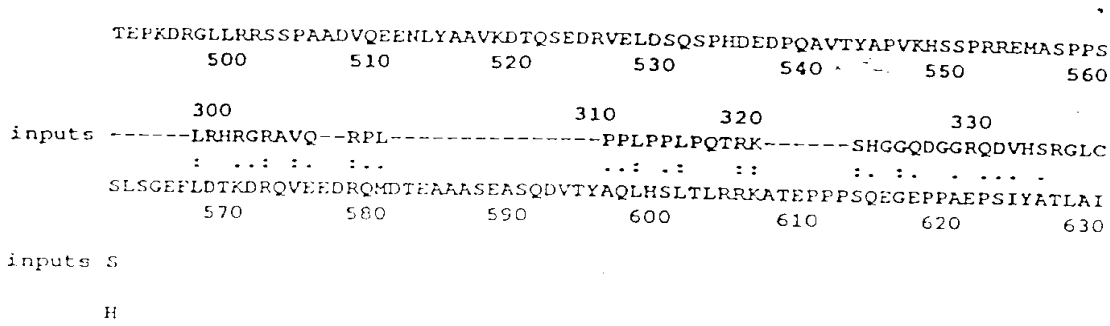


FIGURE 4 cont.

```
Alignments of top-scoring domains:
ig: domain 1 of 2, from 41 to 90: score 4.1, E = 6.1
                  *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                     + vtL+C+          + v  y +  k  ++         r++ +
hT268    41       EKPVTLRCQGP------PGVDLY-RLEKlSSS---------RYQDQ-- 70

                  enlsegrfsissltLtissvekeDsGtYtCvvk-*
                           ++L i   +++ +G Y+C
hT268    71 -------------AVLFIPAMKRSLAGRYRCSY    90
```

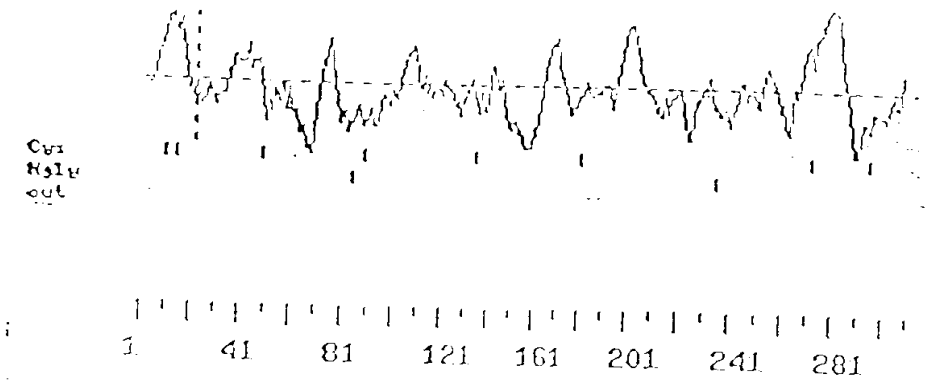
FIGURE 5A

```
ig: domain 2 of 2, from 127 to 182: score 19.1, E = 0.1
                   *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                      G++vtL+C+++    +  ++  y k+g++ +     y+++
        hT268   127    GGDVTLQCQTR---YGFDQFALY-KEGDpAP-----YKNPERWYR-- 167

                   anlsegrfsissltLtissvekeDsGtYtCvv<-*
                             ++++i++v++  sGtY+C
        hT268   163 ----------ASFPIITVTAAHSGTYRCYS    182
```

FIGURE 5B

```
                                                                  M   S   P   A
GAGTCGACCCACGCGTCCGCTTCCCTGCTTGGCCACATAGCTCAGGACTGGGTTGCAGAACC ATG TCT CCA GCC    74

 S   P   T   F   F   C   I   G   L   C   V   L   Q   V   I   Q   T   Q   S   G
TCA CCC ACT TTC TTC TGT ATT GGG CTG TGT GTA CTG CAA GTG ATC CAA ACA CAG AGT GGC   134

 P   L   P   K   P   S   L   Q   A   Q   P   S   S   L   V   P   L   G   G   S
CCA CTC CCC AAA CCT TCC CTC CAG GCT CAG CCC AGT TCC CTG GTA CCC CTG GGT GGA TCA   194

 V   I   L   K   C   Q   G   P   I   D   V   I   L   Y   K   L   E   K   L   E
GTT ATT CTG AGG TGC CAG GGA CCT CCA GAT GTG GAT TTA TAT CGC CTG GAG AAA CTG AAA   254

 P   E   K   Y   E   D   Q   D   E   L   F   I   P   T   M   E   E   S   N   A
CCG GAG AAG TAT GAA GAT CAA GAC TTT CTC TTC ATT CCA ACC ATG GAA AGA AGT AAT GCT   314

 G   R   Y   R   C   S   Y   Q   N   G   S   H   W   S   L   P   S   D   Q   L
GGA CGG TAT CGA TGC TCT TAT CAG AAT GGG AGT CAC TGG TCT CTC CCA AGT GAC CAG CTT   374

 E   L   I   A   T   G   V   Y   A   E   P   S   L   S   A   E   P   S   S   A
GAG CTA ATT GCT ACA GGT GTG TAT GCT AAA CCC TCA CTC TCA GCT GAT CCC AGT TCA GTA   434

 V   I   Q   G   R   D   V   T   L   E   C   S   I   Y   S   F   D   E   F
GTC CCT CAA GGC AGG GAT GTG ACT CTG AAG TGC CAG AGC CCA TAC AGT TTT GAT GAA TTC   494

 V   L   Y   K   E   G   D   T   G   P   Y   E   R   P   E   E   W   Y   R   A
GTT CTA TAC AAA GAA GGG GAT ACT GGG CCT TAT AAG AGA CCT GAG AAA TGG TAC CGG GCC   554

 N   F   P   I   I   T   V   T   A   A   H   S   G   T   Y   R   C   Y   S   F
AAT TTC CCC ATC ATC ACA GTG ACT GCT GCT CAC AGT GGG ACG TAC CGG TGT TAC AGC TTC   614

 S   S   S   S   P   Y   L   W   S   A   P   S   D   P   L   V   L   V   V   T
TCC AGC TCA TCT CCA TAC CTG TGG TCA GCC CCG AGT GAC CCT CTA GTG CTT GTG GTT ACT   674

 G   L   S   A   T   P   S   Q   V   P   T   E   E   S   F   P   V   T   E   S
GGA CTC TCT GCC ACT CCC AGC CAG GTA CCC ACG GAG GAA TCA TTT CCT GTG ACA GAA TCC   734

 S   R   E   P   S   I   L   P   T   N   K   I   S   T   T   F   K   P   M   N
TCC AGG AGA CCT TCC ATC TTA CCC ACA AAC AAA ATA TCT ACA ACT GAA AAG CCT ATG AAT   794

 I   T   A   S   P   E   G   L   S   P   P   I   G   F   A   H   Q   H   Y   A
ATC ACT GCC TCT CCA GAG GGG CTG AGC CCT CCA ATT GGT TTT GCT CAT CAG CAC TAT GCC   854

 K   G   N   L   V   R   I   C   L   G   A   T   I   I   I   I   L   L   G   L
AAG GGG AAT CTG GTC CGG ATA TGC CTT GGT GCC ACG ATT ATA ATA ATT TTG TTG GGG CTT   914

 L   A   E   D   W   H   S   E   K   E   C   L   Q   H   R   M   R   A   L   Q
CTA GCA GAG GAT TGG CAC AGT CGG AAG AAA TGC CTG CAA CAC AGG ATG AGA GCT TTG CAA   974

 R   P   L   P   P   L   P   L   A   •
AGG CCA CTA CCA CCC CTC CCA CTG GCC TAG                                          1004

AAATAACTTGGCTTTCAGCAGAGGGATTGACCAGACATCCATGCACAACCATGGACATCACCACTAGAGCCACAGACAT  1083

GGACATACTCAAGAGTGGGGAGGTTATATAAAAAAAATGAGTGTGGAGAATAAATGCAGAGCCAACAAGGTGAAAAAAAAA  1162

A                                                                               1163
```

FIGURE 6



MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRL
EKLKPEKYEDQDFLFIPTMERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAH
PSSAVPQGRDVTLKCQSPYSFDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAAHSGTYR
CYSFSSSSPYLWSAPSDPLVLVVTGLSATPSQVPTEESFPVTESSRRPSILPTNKISTTE
KPMNITASPEGLSPPIGFAHQHYAKGNLVRICLGATIIIILLGLLAEDWHSRKKCLQHRM
RALQRPLPPLPLA

FIGURE 7

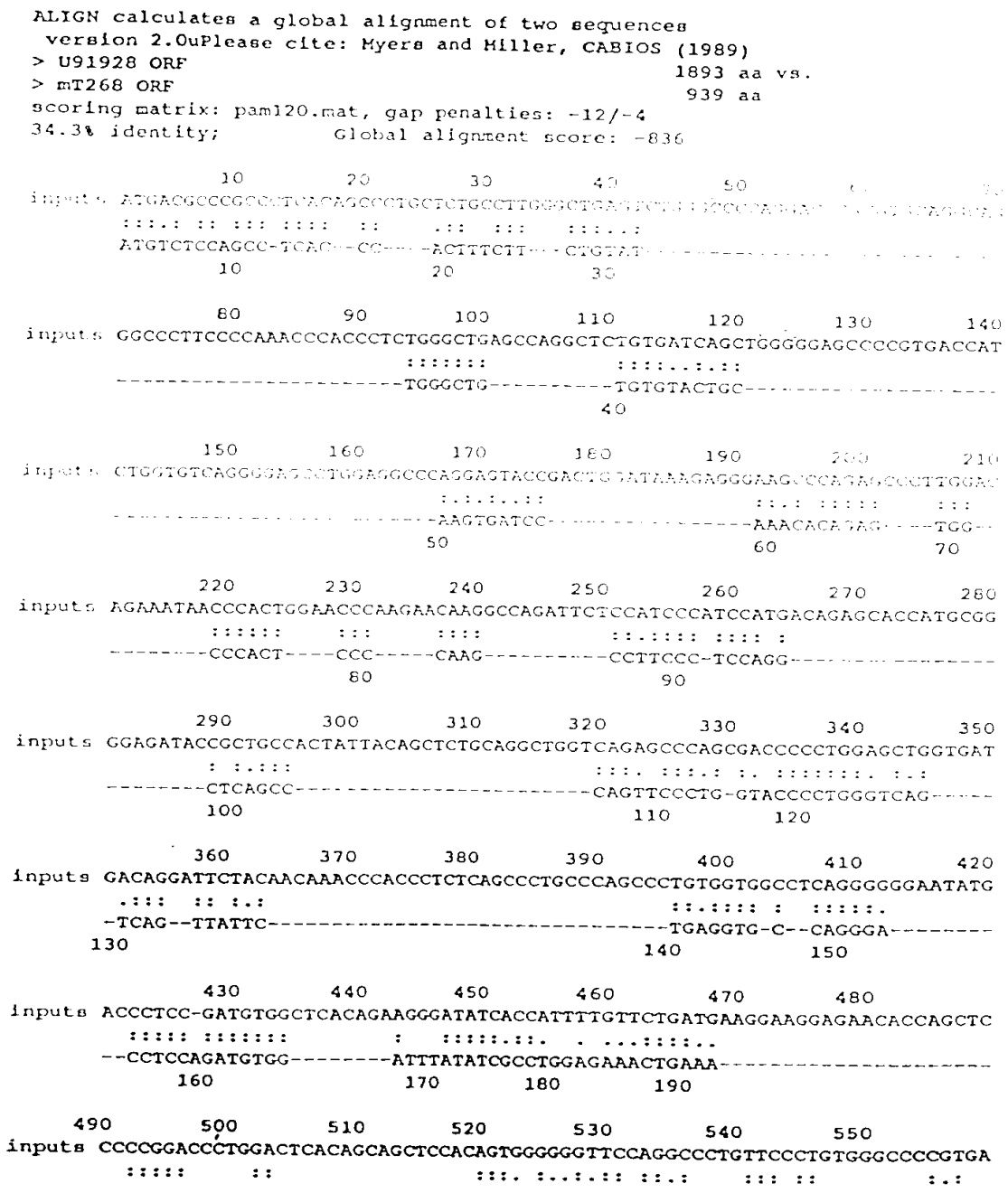

ALIGN calculates a global alignment of two sequences
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> U91928 ORF 1893 aa vs.
> mT268 ORF 939 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
34.3% identity; Global alignment score: -836
inputs
ATGTCTCCAGCC-TCAC--CC----ACTTTCTT---CTGTAT
GGCCCTTCCCCAAACCCACCCTCTGGGCTGAGCCAGGCTCTGTGATCAGCTGGGGGAGCCCCCTGACCAT
TGGGCTG----------TGTGTACTGC
CTGGTGTCAGGGGAGCCTGGAGGCCCAGGAGTACCGACTGTATAAAGAGGGAAGCCCAGAGCCCTTGGAC
AAGTGATCC----------AAACACATAG----TGG--
AGAAATAACCCACTGGAACCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCGG
CCCACT----CCC-----CAAG----------CCTTCCC-TCCAGG----------
GGAGATACCGCTGCCACTATTACAGCTCTGCAGGCTGGTCAGAGCCCAGCGACCCCCTGGAGCTGGTGAT
CTCAGCC----------CAGTTCCCTG-GTACCCCTGGGTCAG------
GACAGGATTCTACAACAAACCCACCCTCTCAGCCCTGCCCAGCCCTGTGGTGGCCTCAGGGGGGAATATG
-TCAG--TTATTC----------TGAGGTG-C--CAGGGA---------
ACCCTCC-GATGTGGCTCACAGAAGGGATATCACCATTTTGTTCTGATGAAGGAAGGAGAACACCAGCTC
--CCTCCAGATGTGG---------ATTTATATCGCCTGGAGAAACTGAAA----------
CCCCGGACCCTGGACTCACAGCAGCTCCACAGTGGGGGGTTCCAGGCCCTGTTCCCTGTGGGCCCCGTGA

FIGURE 8

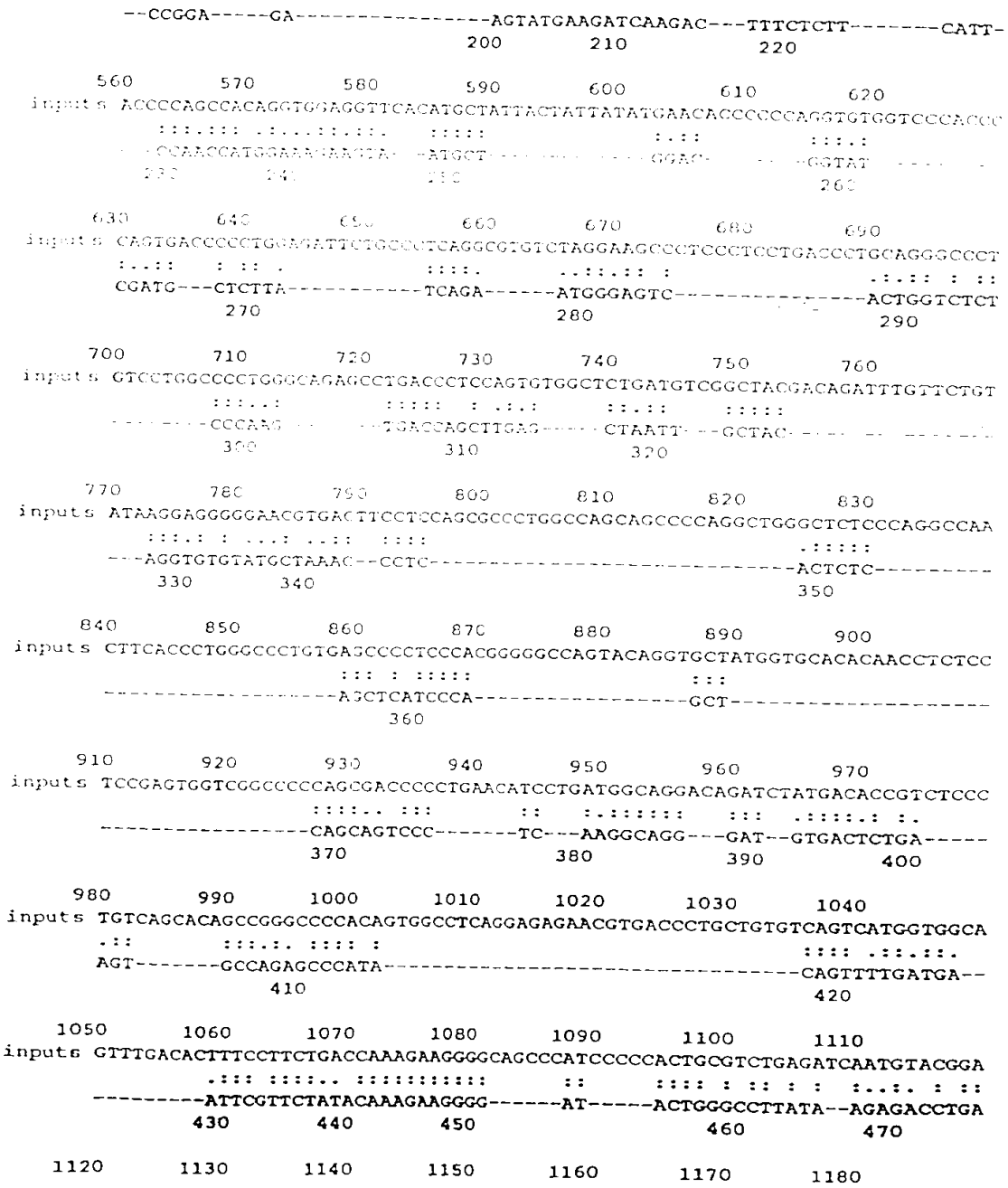


FIGURE 8 cont.

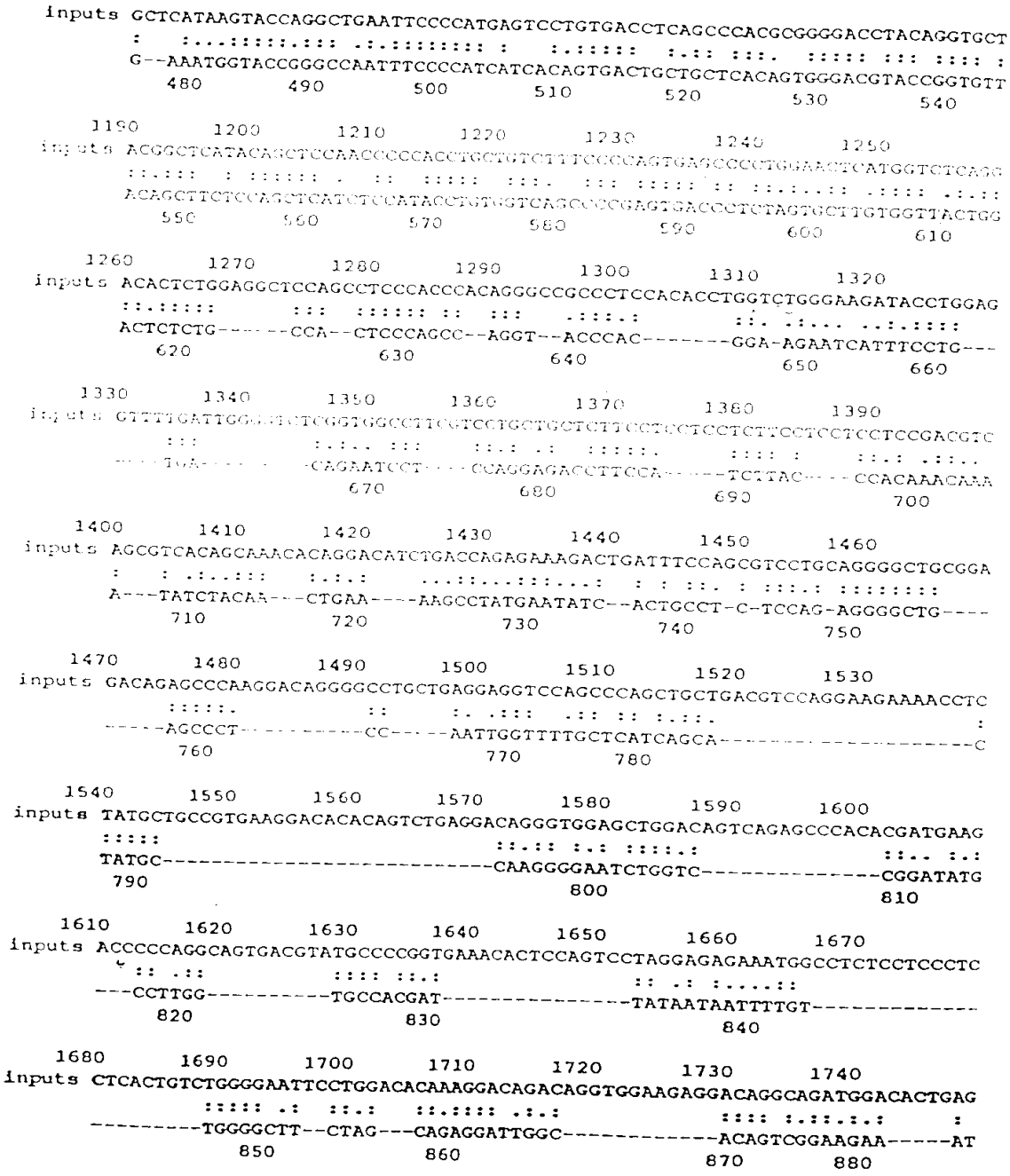


FIGURE 8 cont.

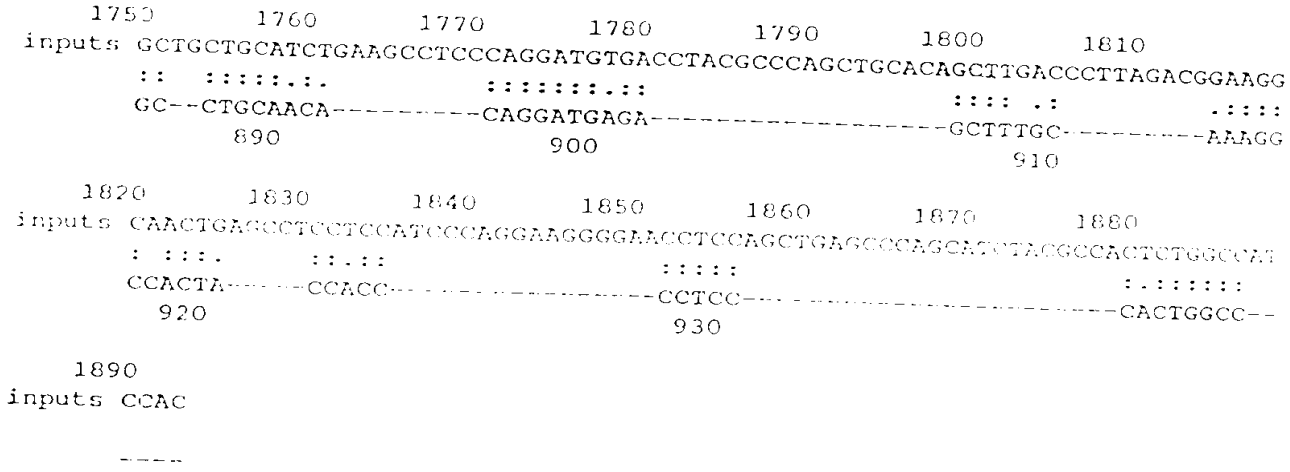


FIGURE 8 cont.

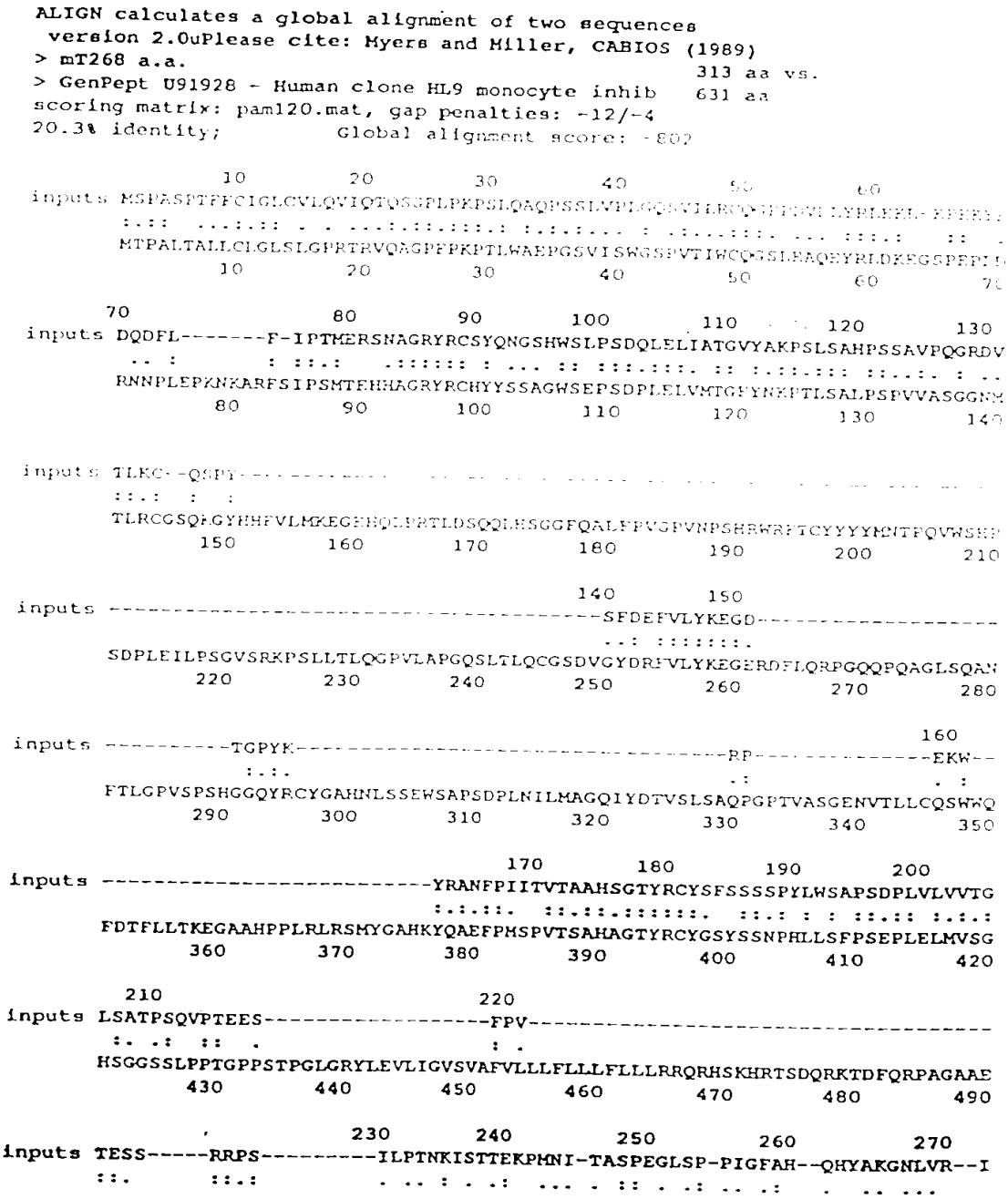

ALIGN calculates a global alignment of two sequences
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> mT268 a.a.
313 aa vs.
> GenPept U91928 - Human clone HL9 monocyte inhib 631 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
20.3% identity; Global alignment score: -802
inputs
MTPALTALLCLGLSLGPRTRVQAGPFPKPTLWAEPGSVISWGSPVTIWCQGSLEAQEYRLDKEGSPEPLD
RNNPLEPKNKARFSIPSMTEHHAGRYRCHYYSSAGWSEPSDPLELVMTGFYNKPTLSALPSPVVASGGNM
TLRCGSQKGYHHFVLMKEGEHQLPRTLDSQQLHSGGFQALFPVGPVNPSHRWRFTCYYYYMNTPQVWSHP
SDPLEILPSGVSRKPSLLTLQGPVLAPGQSLTLQCGSDVGYDRFVLYKEGERDFLQRPGQQPQAGLSQAN
FTLGPVSPSHGGQYRCYGAHNLSSEWSAPSDPLNILMAGQIYDTVSLSAQPGPTVASGENVTLLCQSWWQ
FDTFLLTKEGAAHPPLRLRSMYGAHKYQAEFPMSPVTSAHAGTYRCYGSYSSNPHLLSFPSEPLELMVSG
HSGGSSLPPTGPPSTPGLGRYLEVLIGVSVAFVLLLFLLLFLLLRRQRHSKHRTSDQRKTDFQRPAGAAE
TESS-----RRPS----------ILPTNKISTTEKPMNI-TASPEGLSP-PIGFAH--QHYAKGNLVR--I

FIGURE 9

```
                                                
```

```
Alignments of top-scoring domains:
ig: domain 1 of 2, from 42 to 91: score 10.2, E = 1.4
                   *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                      G+sv L+C+          ++v  y +  k ++          +++e +
          mT268    42    GQSVILRCQGP------PDVDLY-RLEKIKP---------EKYEDQ-- 71

                      anlsegrfsissltLtissvekeDsGtYtCvv<-*
                                L i + e++++G Y+C
          mT268    72 ------------DFLFIPTMERSNAGRYRCSY     91
```

FIGURE 10A

```
ig: domain 2 of 2, from 128 to 183: score 9.6, E = 1.6
                   *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                      G +vtL C++          ++  y k+g++ +        y+r+e  +
        mT268   128   GRDVTLKCQSP---YSFDEFVLY-KEGDtGP-------YKRPEKW-Y 162

                                                  ---
                   anlsegrfsissltLtissvekeDsGtYtCvv<-*
                   +             ++i++v++  sGtY+C
        mT268   163 RA----------NFPIITVTAAHSGTYRCYS     183
```

FIGURE 10B

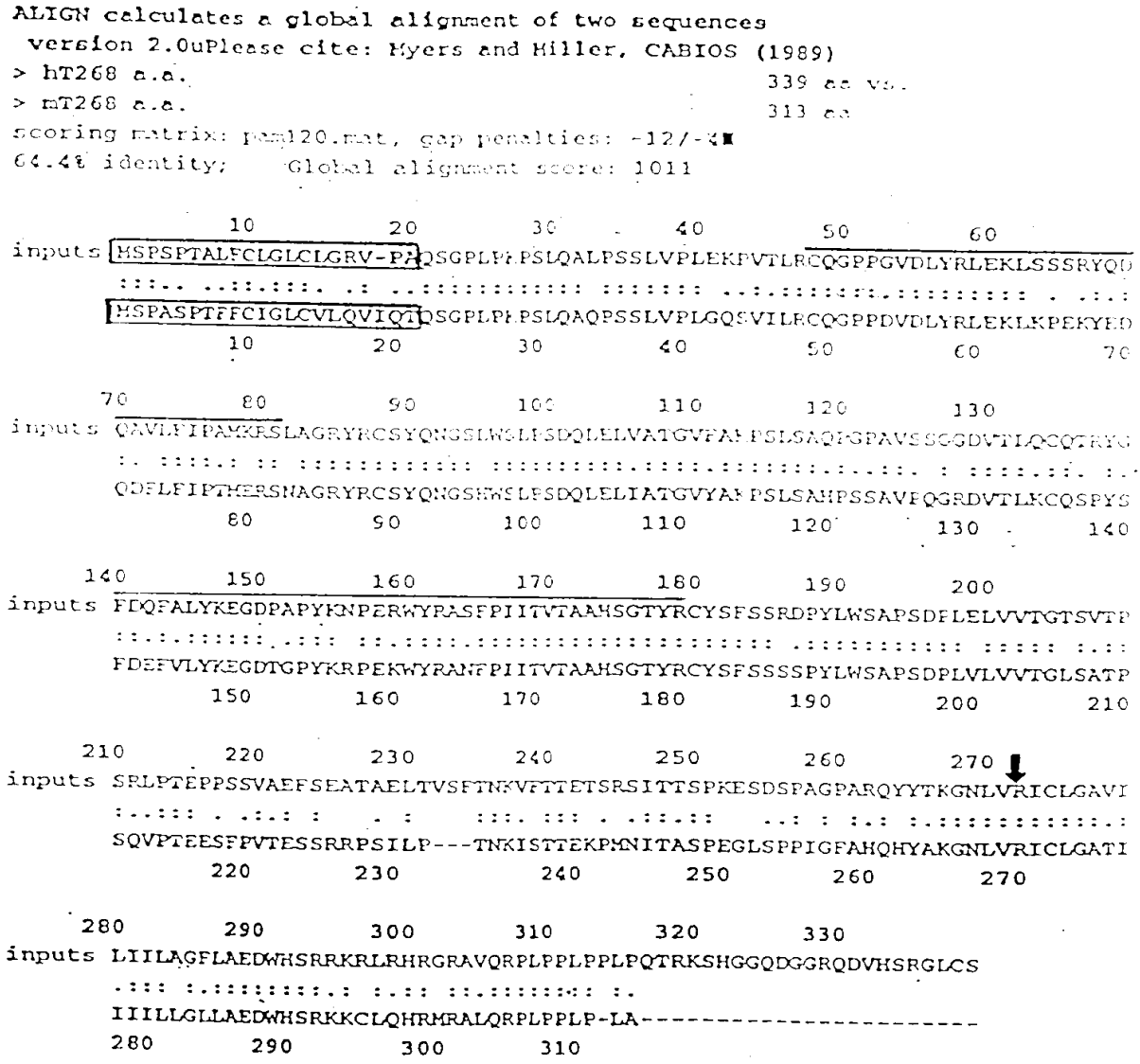

ALIGN calculates a global alignment of two sequences
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> hT268 a.a. 339 aa
> mT268 a.a. 313 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
64.4% identity; Global alignment score: 1011
inputs MSPSPTALFCLGLCLGRV-PAQSGPLPAPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLEKLSSSRYQD
MSPASPTFFCIGLCVLQVIQTQSGPLPAPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRLEKLKPEKYED
inputs QAVLPIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAAPSLSAQPGPAVSSGGDVTLQCQTRYG
QDFLFIPTHERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAAPSLSAHPSSAVFQGRDVTLKCQSPYS
inputs FDQFALYKEGDPAPYKNPERWYRASFPIITVTAAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTGTSVTP
FDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAAHSGTYRCYSFSSSSPYLWSAPSDPLVLVVTGLSATP
inputs SRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRSITTSPKESDSPAGPARQYYTKGNLVRICLGAVI
SQVPTEESFPVTESSRRPSILP---TNKISTTEKPMNITASPEGLSPPIGFAHQHYAKGNLVRICLGATI
inputs LIILAGFLAEDWHSRRKRLRHRGRAVQRPLPPLPPLPQTRKSHGGQDGGRQDVHSRGLCS
IIILLGLLAEDWHSRKKCLQHRMRALQRPLPPLP-LA----------

FIGURE 11

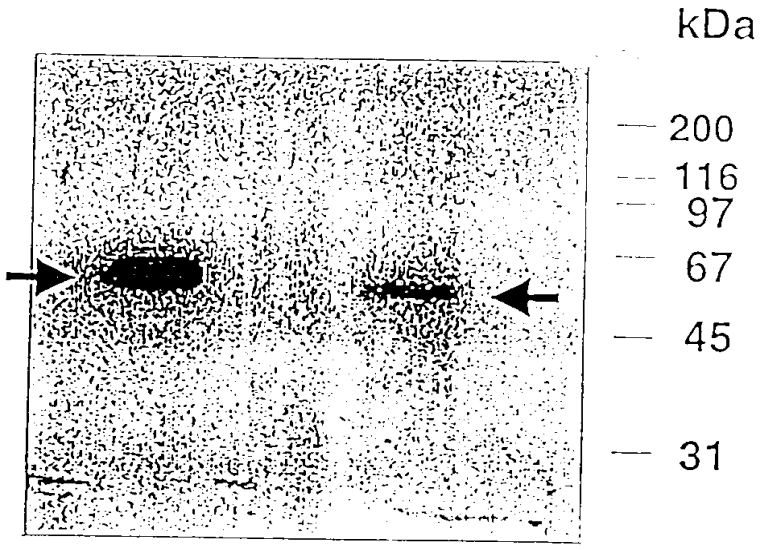


FIGURE 12

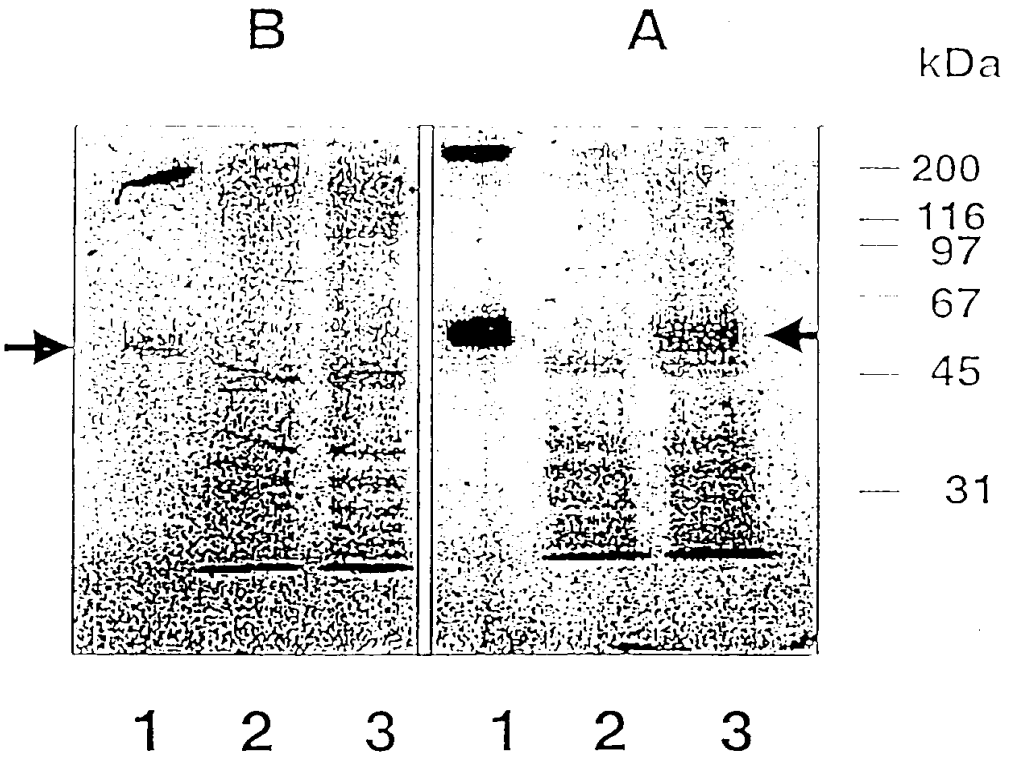


FIGURE 13

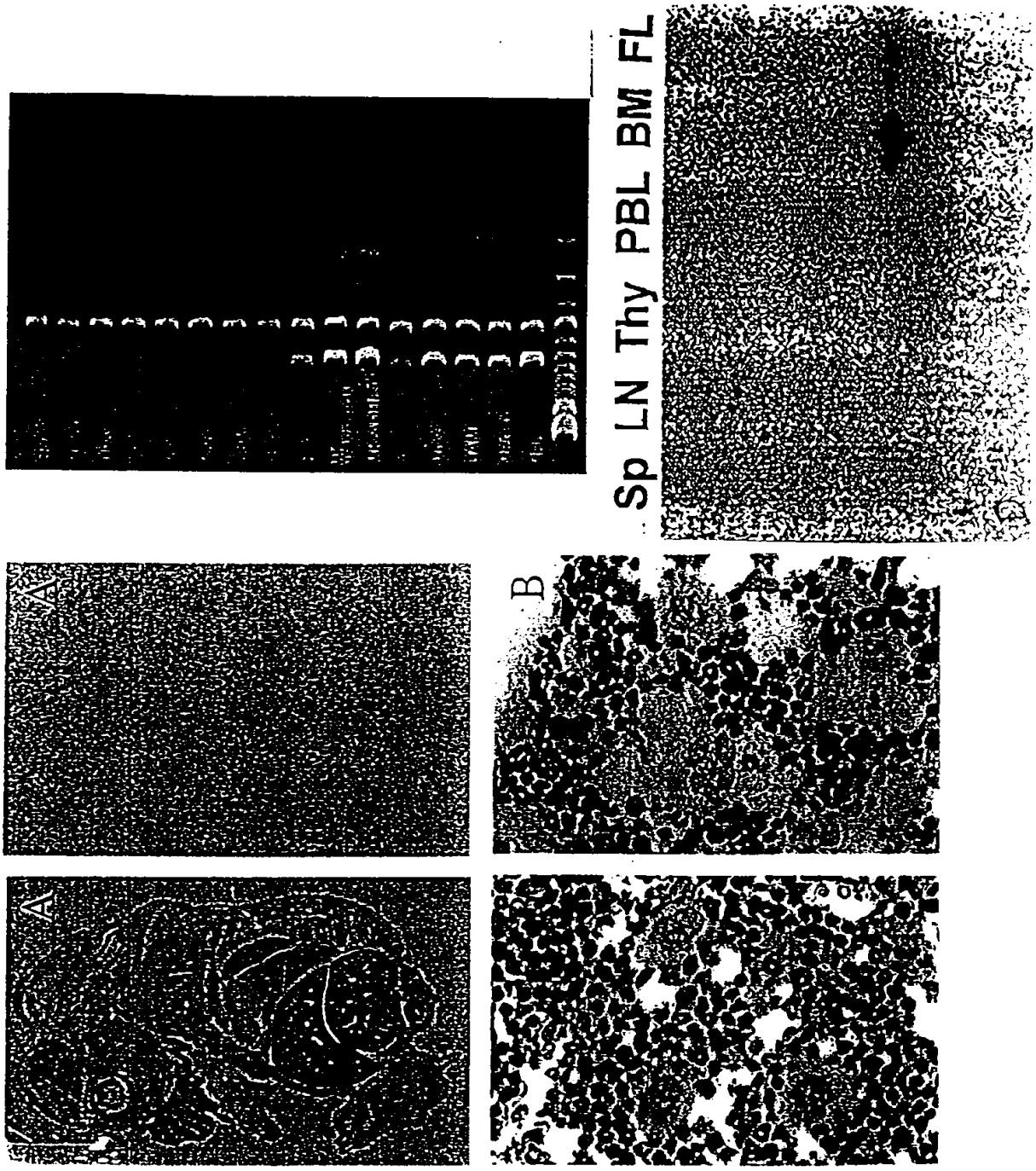


FIGURE 14

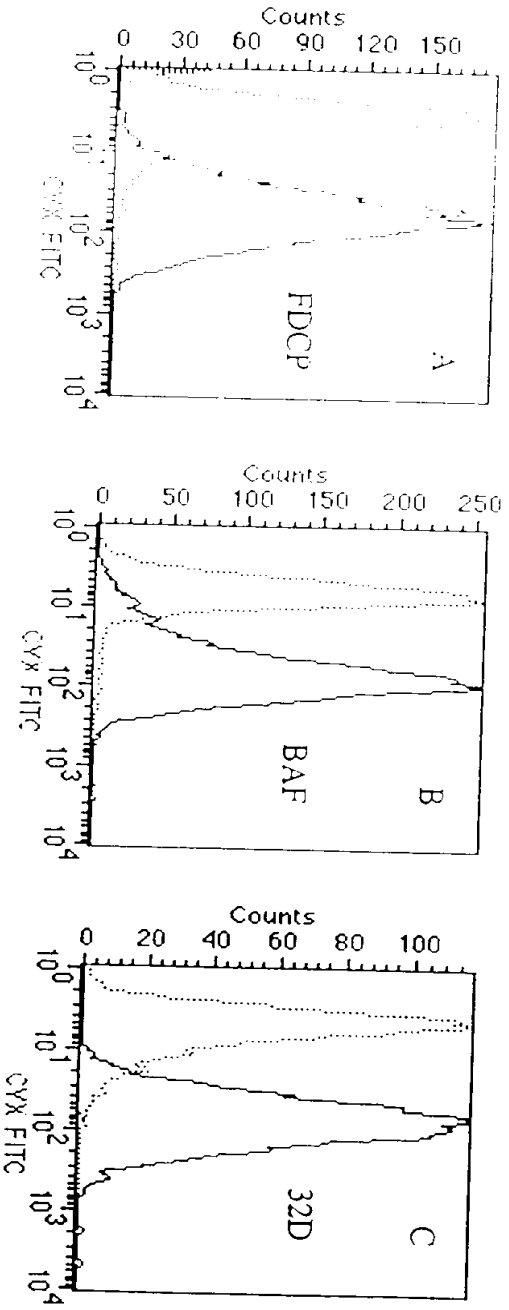

Counts
0 30 60 90 120 150
CYX FITC
FDCP
A
Counts
0 50 100 150 200 250
CYX FITC
BAF
B
Counts
0 20 40 60 80 100
CYX FITC
32D
C

FIGURE 15

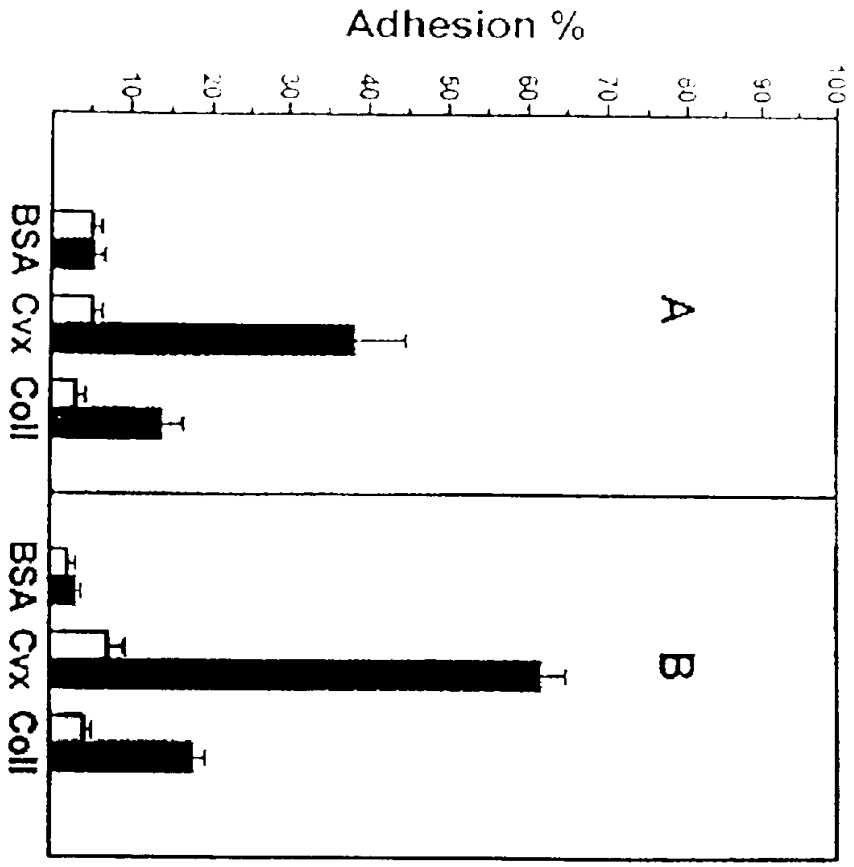

Adhesion %
10
20
30
40
50
60
70
80
90
100
BSA
Cvx
Coll
A
BSA
Cvx
Coll
B

FIGURE 16

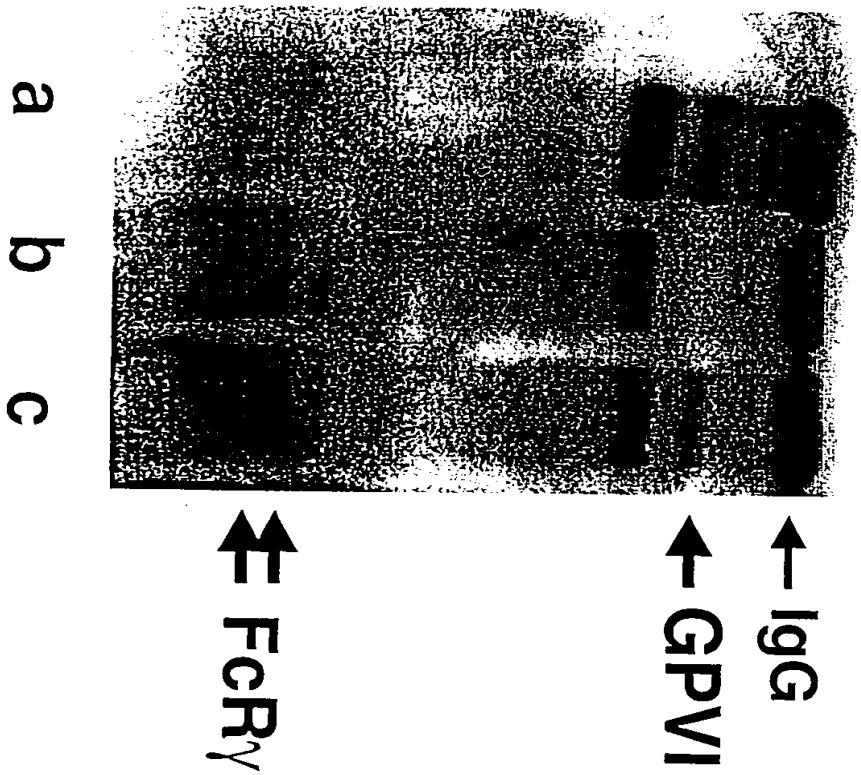


FIGURE 17

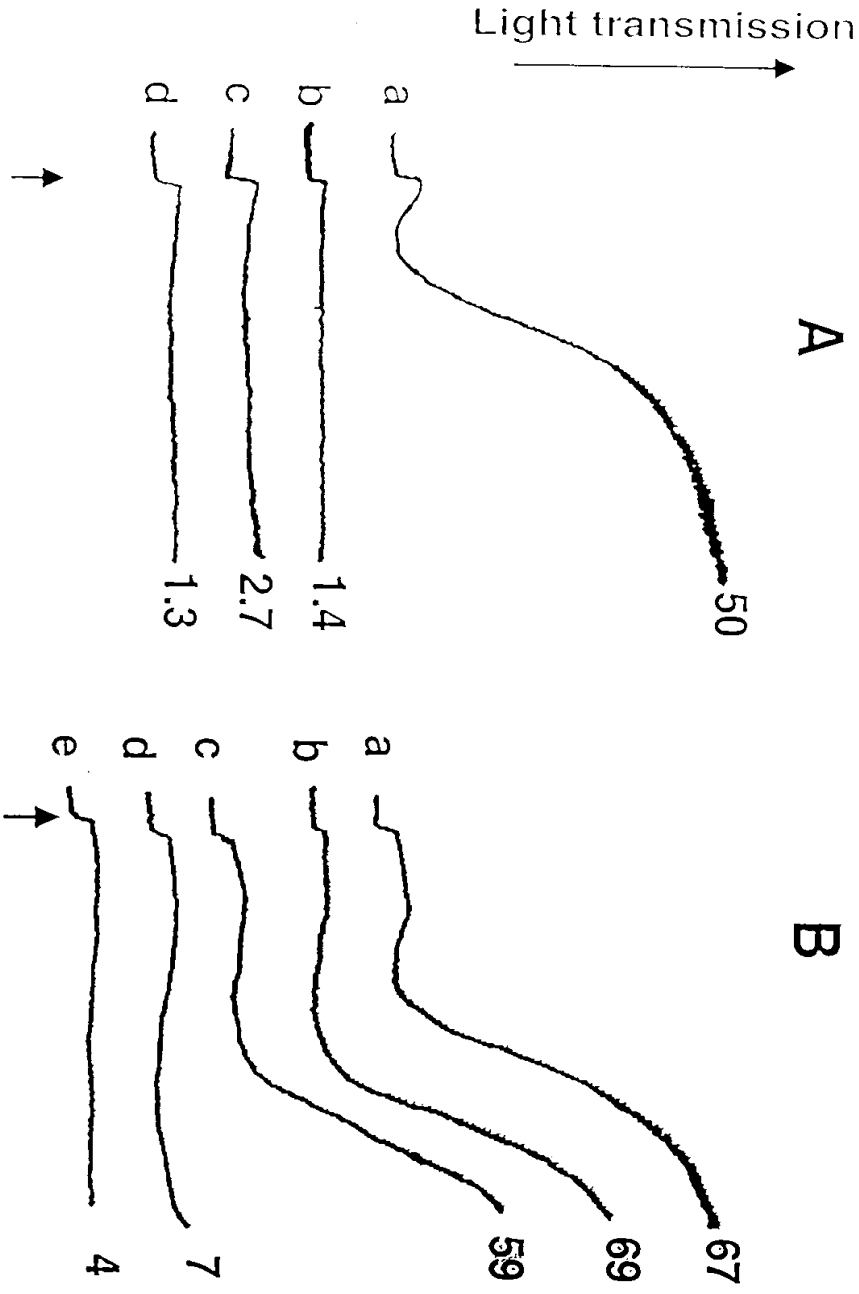


FIGURE 18

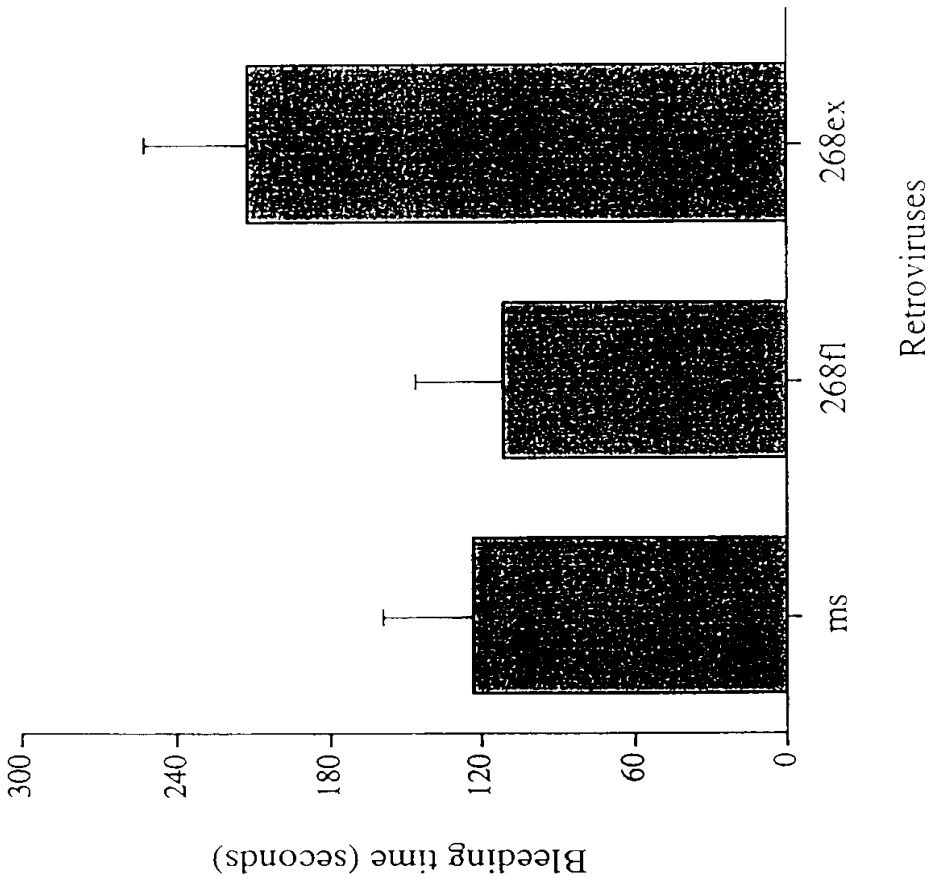

Bleeding time (seconds)
300
240
180
120
60
0
ms
268fl
268ex
Retroviruses

FIGURE 19